

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/512,5810  
Source: 1Fw16  
Date Processed by STIC: 1/4/05

# ***ENTERED***

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 09/512,5810

CRF Edit Date: 1/4/05  
Edited by: [Signature]

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted:    invalid beginning/end-of-file text ;    page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

\_\_\_ Other:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



IFW16

## RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/09/512,581D

TIME: 17:45:24

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01042005\I512581D.raw

3 <110> APPLICANT: Soto, Ana M.  
 4 Sonnenschein, Carlos  
 5 Geck, Peter  
 6 Szelei, Jozsef  
 8 <120> TITLE OF INVENTION: NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND  
 USES  
 9 THEREOF  
 11 <130> FILE REFERENCE: 34724-026  
 13 <140> CURRENT APPLICATION NUMBER: US 09/512,581D  
 14 <141> CURRENT FILING DATE: 2000-02-24  
 16 <150> PRIOR APPLICATION NUMBER: US 60/121,461  
 17 <151> PRIOR FILING DATE: 1999-02-24  
 19 <160> NUMBER OF SEQ ID NOS: 72  
 21 <170> SOFTWARE: PatentIn version 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 5271  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (66)..(4238)  
 32 <400> SEQUENCE: 1  
 33 ccggagagcc ccggagtgcg cggagtagcg agtcggcaac ccggaggggt agaaatattt 60  
 35 ctgtc atg gct cat tca aag act agg acc aat gat gga aaa att aca tat 110  
 36 Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr  
 37 1 5 10 15  
 39 ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158  
 40 Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met  
 41 20 25 30  
 43 gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206  
 44 Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln  
 45 35 40 45  
 47 gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254  
 48 Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu  
 49 50 55 60  
 51 gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg 302  
 52 Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu  
 53 65 70 75  
 55 gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350  
 56 Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala  
 57 80 85 90 95  
 59 cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398  
 60 Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr  
 61 100 105 110

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63	aga	cag	ttg	aag	ggg	cta	gag	gat	aca	aag	agc	cca	caa	ttc	aat	agg	446
64	Arg	Gln	Leu	Lys	Gly	Leu	Glu	Asp	Thr	Lys	Ser	Pro	Gln	Phe	Asn	Arg	
65				115					120					125			
67	tat	ttt	tat	tta	ctt	gag	aac	att	gct	tgg	gtc	aag	tca	tat	aac	ata	494
68	Tyr	Phe	Tyr	Leu	Leu	Glu	Asn	Ile	Ala	Trp	Val	Lys	Ser	Tyr	Asn	Ile	
69			130					135					140				
71	tgc	ttt	gag	tta	gaa	gat	agc	aat	gaa	att	ttc	acc	cag	cta	tac	aga	542
72	Cys	Phe	Glu	Leu	Glu	Asp	Ser	Asn	Glu	Ile	Phe	Thr	Gln	Leu	Tyr	Arg	
73		145					150					155					
75	acc	tta	ttt	tca	gtt	ata	aac	aat	ggc	cac	aat	cag	aaa	gtc	cat	atg	590
76	Thr	Leu	Phe	Ser	Val	Ile	Asn	Asn	Gly	His	Asn	Gln	Lys	Val	His	Met	
77	160					165				170					175		
79	cac	atg	gta	gac	ctt	atg	agc	tct	att	att	tgt	gaa	ggg	gat	aca	gtg	638
80	His	Met	Val	Asp	Leu	Met	Ser	Ser	Ile	Ile	Cys	Glu	Gly	Asp	Thr	Val	
81				180						185					190		
83	tct	cag	gag	ctt	ttg	gat	acg	gtt	tta	gta	aat	ctg	gtac	cct	gct	cat	686
84	Ser	Gln	Glu	Leu	Leu	Asp	Thr	Val	Leu	Val	Asn	Leu	Val	Pro	Ala	His	
85			195					200					205				
87	aag	aat	tta	aac	aag	caa	gca	tat	gat	ttg	gca	aag	gct	tta	ctg	aag	734
88	Lys	Asn	Leu	Asn	Lys	Gln	Ala	Tyr	Asp	Leu	Ala	Lys	Ala	Leu	Leu	Lys	
89			210					215					220				
91	agg	aca	gct	caa	gct	att	gag	cca	tat	att	acc	act	ttt	ttt	aat	cag	782
92	Arg	Thr	Ala	Gln	Ala	Ile	Glu	Pro	Tyr	Ile	Thr	Thr	Phe	Phe	Asn	Gln	
93			225					230					235				
95	gtt	ctg	atg	ctt	ggg	aaa	aca	tct	atc	agc	gat	ttg	tca	gag	cat	gtc	830
96	Val	Leu	Met	Leu	Gly	Lys	Thr	Ser	Ile	Ser	Asp	Leu	Ser	Glu	His	Val	
97	240				245					250				255			
99	ttt	gac	tta	att	ttg	gag	ctc	tac	aat	att	gat	agt	cat	ttg	ctg	ctc	878
100	Phe	Asp	Leu	Ile	Leu	Glu	Leu	Tyr	Asn	Ile	Asp	Ser	His	Leu	Leu	Leu	
101				260						265				270			
103	tct	gtt	tta	ccc	cag	ctt	gaa	ttt	aaa	tta	aag	agc	aat	gat	aat	gag	926
104	Ser	Val	Leu	Pro	Gln	Leu	Glu	Phe	Lys	Leu	Lys	Ser	Asn	Asp	Asn	Glu	
105				275					280					285			
107	gag	cgc	cta	caa	gtt	gtt	aaa	cta	ctg	gca	aaa	atg	ttt	ggg	gca	aag	974
108	Glu	Arg	Leu	Gln	Val	Val	Lys	Leu	Leu	Ala	Lys	Met	Phe	Gly	Ala	Lys	
109			290					295					300				
111	gat	tca	gaa	ttg	gct	tct	caa	aac	aag	cca	ctt	tgg	cag	tgc	tac	ttg	1022
112	Asp	Ser	Glu	Leu	Ala	Ser	Gln	Asn	Lys	Pro	Leu	Trp	Gln	Cys	Tyr	Leu	
113			305				310						315				
115	ggc	agg	ttt	aat	gat	atc	cat	gta	cca	atc	cgc	ctg	gaa	tgt	gtg	aaa	1070
116	Gly	Arg	Phe	Asn	Asp	Ile	His	Val	Pro	Ile	Arg	Leu	Glu	Cys	Val	Lys	
117	320					325					330				335		
119	ttt	gct	agc	cat	tgt	ctc	atg	aac	cat	cct	gat	tta	gca	aaa	gac	tta	1118
120	Phe	Ala	Ser	His	Cys	Leu	Met	Asn	His	Pro	Asp	Leu	Ala	Lys	Asp	Leu	
121				340						345				350			
123	aca	gag	tat	ctt	aaa	gtg	agg	tca	cat	gac	cct	gag	gaa	gct	att	aga	1166
124	Thr	Glu	Tyr	Leu	Lys	Val	Arg	Ser	His	Asp	Pro	Glu	Glu	Ala	Ile	Arg	
125				355						360				365			
127	cat	gat	gtt	att	gtg	tca	ata	gtt	aca	gct	gct	aaa	aag	gat	att	ctt	1214

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128	His	Asp	Val	Ile	Val	Ser	Ile	Val	Thr	Ala	Ala	Lys	Lys	Asp	Ile	Leu	
129			370					375					380				
131	ctg	gtc	aat	gat	cac	tta	ctt	aat	ttt	gtg	aga	gag	aga	aca	tta	gac	1262
132	Leu	Val	Asn	Asp	His	Leu	Leu	Asn	Phe	Val	Arg	Glu	Arg	Thr	Leu	Asp	
133			385					390					395				
135	aaa	cga	tgg	aga	gta	cgc	aaa	gaa	gcc	atg	atg	gga	ctt	gcc	caa	att	1310
136	Lys	Arg	Trp	Arg	Val	Arg	Lys	Glu	Ala	Met	Met	Gly	Leu	Ala	Gln	Ile	
137	400					405					410					415	
139	tat	aag	aaa	tat	gct	tta	cag	tca	gca	gct	gga	aaa	gat	gct	gca	aaa	1358
140	Tyr	Lys	Lys	Tyr	Ala	Leu	Gln	Ser	Ala	Ala	Gly	Lys	Asp	Ala	Ala	Lys	
141					420					425					430		
143	cag	ata	gca	tgg	atc	aaa	gac	aaa	ttg	cta	cat	ata	tat	tat	caa	aat	1406
144	Gln	Ile	Ala	Trp	Ile	Lys	Asp	Lys	Leu	Leu	His	Ile	Tyr	Tyr	Gln	Asn	
145			435						440						445		
147	agt	att	gat	gat	cga	cta	ctt	gtt	gaa	cgg	atc	ttt	gct	caa	tac	atg	1454
148	Ser	Ile	Asp	Arg	Leu	Leu	Val	Glu	Arg	Ile	Phe	Ala	Gln	Tyr	Met		
149			450					455					460				
151	gtt	cct	cac	aat	tta	gaa	act	aca	gaa	cgg	atg	aaa	tgc	tta	tat	tac	1502
152	Val	Pro	His	Asn	Leu	Glu	Thr	Thr	Glu	Arg	Met	Lys	Cys	Leu	Tyr	Tyr	
153			465					470					475				
155	ttg	tat	gcc	aca	ctg	gat	tta	aat	gct	gtg	aaa	gca	ttg	aat	gaa	atg	1550
156	Leu	Tyr	Ala	Thr	Leu	Asp	Leu	Asn	Ala	Val	Lys	Ala	Leu	Asn	Glu	Met	
157	480					485					490					495	
159	tgg	aaa	tgt	caa	aat	ctg	ctc	cga	cat	caa	gta	aag	gat	ttg	ctt	gac	1598
160	Trp	Lys	Cys	Gln	Asn	Leu	Leu	Arg	His	Gln	Val	Lys	Asp	Leu	Leu	Asp	
161					500					505					510		
163	ttg	att	aag	caa	ccc	aaa	aca	gat	gcc	agt	gtc	aag	gcc	ata	ttt	tca	1646
164	Leu	Ile	Lys	Gln	Pro	Lys	Thr	Asp	Ala	Ser	Val	Lys	Ala	Ile	Phe	Ser	
165			515						520						525		
167	aaa	gtg	atg	gtt	att	aca	aga	aat	tta	cct	gat	cct	ggg	aag	gct	cag	1694
168	Lys	Val	Met	Val	Ile	Thr	Arg	Asn	Leu	Pro	Asp	Pro	Gly	Lys	Ala	Gln	
169			530					535					540				
172	gat	ttc	atg	aag	aaa	ttc	aca	cag	gtg	tta	gaa	gat	gat	gag	aaa	ata	1742
173	Asp	Phe	Met	Lys	Lys	Phe	Thr	Gln	Val	Leu	Glu	Asp	Asp	Glu	Lys	Ile	
174			545				550						555				
176	aga	aag	cag	tta	gaa	gta	ctt	gtt	agt	cca	aca	tgc	tcc	tgc	aag	cag	1790
177	Arg	Lys	Gln	Leu	Glu	Val	Leu	Val	Ser	Pro	Thr	Cys	Ser	Cys	Lys	Gln	
178	560					565					570					575	
180	gct	gaa	ggg	tgt	gtg	cgt	gaa	ata	act	aag	aag	ttg	ggc	aac	ccc	aaa	1838
181	Ala	Glu	Gly	Cys	Val	Arg	Glu	Ile	Thr	Lys	Lys	Leu	Gly	Asn	Pro	Lys	
182					580					585					590		
184	cag	cct	aca	aat	cct	ttc	ctg	gaa	atg	atc	aag	ttt	ctc	ttg	gag	agg	1886
185	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met	Ile	Lys	Phe	Leu	Leu	Glu	Arg	
186			595						600						605		
188	ata	gca	cct	gtg	cac	ata	gat	acc	gaa	tct	atc	agt	gct	ctt	att	aaa	1934
189	Ile	Ala	Pro	Val	His	Ile	Asp	Thr	Glu	Ser	Ile	Ser	Ala	Leu	Ile	Lys	
190			610					615							620		
192	caa	gtg	aac	aaa	tca	ata	gat	gga	aca	gca	gat	gat	gaa	gat	gag	ggg	1982
193	Gln	Val	Asn	Lys	Ser	Ile	Asp	Gly	Thr	Ala	Asp	Asp	Glu	Asp	Glu	Gly	

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194	625	630	635	
196	gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta	2030		
197	Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val			
198	640 645 650 655			
200	ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078		
201	Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu			
202	660 665 670			
204	tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct	2126		
205	Ser Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala			
206	675 680 685			
208	gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt	2174		
209	Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe			
210	690 695 700			
212	cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa	2222		
213	Pro His Ile Arg Ser Ala Leu Pro Val Leu His His Lys Ser Lys			
214	705 710 715			
216	aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg	2270		
217	Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala			
218	720 725 730 735			
220	ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg	2318		
221	Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu			
222	740 745 750			
224	cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg	2366		
225	His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu			
226	755 760 765			
229	gtt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct	2414		
230	Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala			
231	770 775 780			
233	cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg	2462		
234	Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met			
235	785 790 795			
237	aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat	2510		
238	Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp			
239	800 805 810 815			
241	gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg	2558		
242	Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met			
243	820 825 830			
245	atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga	2606		
246	Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly			
247	835 840 845			
249	act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac	2654		
250	Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp			
251	850 855 860			
253	ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga	2702		
254	Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg			
255	865 870 875			
257	ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac	2750		
258	Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr			
259	880 885 890 895			

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261 cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc 2798
262 His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile
263          900          905          910
265 aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac 2846
266 Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His
267          915          920          925
269 aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt 2894
270 Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys
271          930          935          940
273 gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg 2942
274 Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg
275          945          950          955
277 caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag 2990
278 Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln
279 960          965          970          975
281 cat gca gct gtt agt gaa aaa tta ttg tct ctt cta ccagag tat gtt 3038
282 His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val
283          980          985          990
286 gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa 3086
287 Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys
288          995          1000          1005
290 gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt 3134
291 Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe
292          1010          1015          1020
294 gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt 3182
295 Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe
296          1025          1030          1035
298 atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga 3230
299 Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly
300 1040          1045          1050          1055
302 cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt 3278
303 Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val
304          1060          1065          1070
306 gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct 3326
307 Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser
308          1075          1080          1085
310 cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag 3374
311 Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys
312          1090          1095          1100
314 aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt 3422
315 Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe
316          1105          1110          1115
318 ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac 3470
319 Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn
320 1120          1125          1130          1135
322 aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga 3518
323 Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg
324          1140          1145          1150
326 atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct 3566

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/512,581D

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Input Set : A:\PTO.AMC.txt

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42  
Seq#:1; Line(s) 43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62  
Seq#:1; Line(s) 63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82  
Seq#:1; Line(s) 83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101  
Seq#:1; Line(s) 102,103,104,105,106,107,108,109,110,111,112,113,114,115,116  
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Seq#:1; Line(s) 132,133,134,135,136,137,138,139,140,141,142,143,144,145,146  
Seq#:1; Line(s) 147,148,149,150,151,152,153,154,155,156,157,158,159,160,161  
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Seq#:1; Line(s) 179,180,181,182,183,184,185,186,187,188,189,190,191,192,193  
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**RAW SEQUENCE LISTING ERROR SUMMARY**  
PATENT APPLICATION: US/09/512,581D

DATE: 01/04/2005  
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**VERIFICATION SUMMARY**

DATE: 01/04/2005

PATENT APPLICATION: US/09/512,581D

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IFW16

## RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/09/512,581D

TIME: 10:00:22

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Output Set: N:\CRF4\01042005\I512581D.raw

3 <110> APPLICANT: Soto, Ana M.  
 4       Sonnenschein, Carlos  
 5       Geck, Peter  
 6       Szelei, Jozsef  
 8 <120> TITLE OF INVENTION: NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL PROLIFERATION AND  
 USES  
 9       THEREOF  
 11 <130> FILE REFERENCE: 34724-026  
 13 <140> CURRENT APPLICATION NUMBER: US 09/512,581D  
 14 <141> CURRENT FILING DATE: 2000-02-24  
 16 <150> PRIOR APPLICATION NUMBER: US 60/121,461  
 17 <151> PRIOR FILING DATE: 1999-02-24  
 19 <160> NUMBER OF SEQ ID NOS: 72  
 21 <170> SOFTWARE: PatentIn version 3.3

## ERRORED SEQUENCES

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13

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/512,581D

DATE: 01/04/2005  
TIME: 10:00:24

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Output Set: N:\CRF4\01042005\I512581D.raw

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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**VERIFICATION SUMMARY**

DATE: 01/04/2005

PATENT APPLICATION: US/09/512,581D

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L:2241 M:254 E: No. of Bases conflict, this line has no nucleotides.